



#6

## SEQUENCE LISTING

&lt;110&gt; Sacktor, Todd C.

&lt;120&gt; A MEMORY ENHANCING PROTEIN

&lt;130&gt; The Research Foundation Albany

&lt;140&gt; 09/839,073

&lt;141&gt; 2001-04-20

&lt;160&gt; 4

&lt;170&gt; PatentIn Ver. 2.1

&lt;210&gt; 1

&lt;211&gt; 2058

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (444)..(1670)

&lt;220&gt;

&lt;221&gt; unsure

&lt;222&gt; (522)

&lt;223&gt; r at position 522 is g or a

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aagccgacgc agcatcagct cgtcaacggg aaggaagatg cctccctgca cgcccgccgc 180  
gcacagagca taaagaatct gcgctgagga ggcaggagaa gaaagccgaa tctatctacc 240  
gccggggagc cagaagatgg aggaagctgt accgtgccaa cggccacctc ttccaagcca 300  
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ggcaaggcta caggtgcata aactgcaaac tgctgggtcca taagcgctgc cacggcctcg 420  
tcccgtgac ctgcaggaag cat atg gat tct gtc atg cct tcc caa gag cct 473  
Met Asp Ser Val Met Pro Ser Gln Glu Pro  
1 5 10

cca gta gac gac aag aac gag gac gcc gac ctt cct tcc gag gag aca 521  
Pro Val Asp Asp Lys Asn Glu Asp Ala Asp Leu Pro Ser Glu Glu Thr  
15 20 25

rat gga att gct tac att tcc tca tcc cgg aag cat gac agc att aaa 569  
Xaa Gly Ile Ala Tyr Ile Ser Ser Ser Arg Lys His Asp Ser Ile Lys  
30 35 40

gac gac tcg gag gac ctt aag cca gtt atc gat ggg atg gat gga atc 617  
Asp Asp Ser Glu Asp Leu Lys Pro Val Ile Asp Gly Met Asp Gly Ile  
45 50 55

aaa atc tct cag ggg ctt ggg ctg cag gac ttt gac cta atc aga gtc 665  
Lys Ile Ser Gln Gly Leu Gly Leu Gln Asp Phe Asp Leu Ile Arg Val  
60 65 70

atc Ile 75	ggg Gly	cgc Arg	ggg Gly	agc Ser	tac Tyr 80	gcc Ala	aag Lys	gtt Val	ctc Leu	ctg Leu 85	gtg Val	cgg Arg	ttg Leu	aag Lys	aag Lys 90	713
aat Asn	gac Asp	caa Gln	att Ile	tac Tyr 95	gcc Ala	atg Met	aaa Lys	gtg Val	gtg Val 100	aag Lys	aaa Lys	gag Glu	ctg Leu	gtg Val 105	cat His	761
gat Asp	gac Asp	gag Glu	gat Asp 110	att Ile	gac Asp	tgg Trp	gta Val	cag Gln 115	aca Thr	gag Glu	aag Lys	cac His	gtg Val 120	ttt Phe	gag Glu	809
cag Gln	gca Ala	tcc Ser 125	agc Ser	aac Asn	ccc Pro	ttc Phe	ctg Leu 130	gtc Val	gga Gly	tta Leu	cac His	tcc Ser 135	tgc Cys	ttc Phe	cag Gln	857
acg Thr 140	aca Thr	agt Ser	cgg Arg	ttg Leu	ttc Phe	ctg Leu 145	gtc Val	att Ile	gag Glu	tac Tyr	gtc Val 150	aac Asn	ggc Gly	ggg Gly	gac Asp	905
ctg Leu 155	atg Met	ttc Phe	cac His	atg Met	cag Gln 160	agg Arg	cag Gln	agg Arg	aag Lys	ctc Leu 165	cct Pro	gag Glu	gag Glu	cac His	gcc Ala 170	953
agg Arg	ttc Phe	tac Tyr	gcg Ala	gcc Ala 175	gag Glu	atc Ile	tgc Cys	atc Ile	gcc Ala 180	ctc Leu	aac Asn	ttc Phe	ctg Leu	cac His 185	gag Glu	1001
agg Arg	ggg Gly	atc Ile	atc Ile 190	tac Tyr	agg Arg	gac Asp	ctg Leu	aag Lys 195	ctg Leu	gac Asp	aac Asn	gtc Val	ctc Leu 200	ctg Leu	gat Asp	1049
gcg Ala	gac Asp	ggg Gly 205	cac His	atc Ile	aag Lys	ctc Leu	aca Thr 210	gac Asp	tac Tyr	ggc Gly	atg Met	tgc Cys 215	aag Lys	gaa Glu	ggc Gly	1097
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ccg Pro	ttc Phe	gac Asp	atc Ile 270	atc Ile	acc Thr	gac Asp	aac Asn	ccg Pro 275	gac Asp	atg Met	aac Asn	aca Thr	gag Glu 280	gac Asp	tac Tyr	1289
ctt Leu	ttc Phe	caa Gln 285	gtg Val	atc Ile	ctg Leu	gag Glu	aag Lys 290	ccc Pro	atc Ile	cgg Arg	atc Ile	ccc Pro 295	cgg Arg	ttc Phe	ctg Leu	1337
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aaa Lys 315	gag Glu	agg Arg	ctc Leu	ggc Gly	tgc Cys 320	cgg Arg	cca Pro	cag Gln	act Thr	gga Gly 325	ttt Phe	tct Ser	gac Asp	atc Ile	aag Lys 330	1433

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 Ser His Ala Phe Phe Arg Ser Ile Asp Trp Asp Leu Leu Glu Lys Lys  
 335 340 345  
 cag gcg ctc cct cca ttc cag cca cag atc aca gac gac tac ggt ctg 1529  
 Gln Ala Leu Pro Pro Phe Gln Pro Gln Ile Thr Asp Asp Tyr Gly Leu  
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 gac aac ttt gac aca cag ttc acc agc gag ccc gtg cag ctg acc cca 1577  
 Asp Asn Phe Asp Thr Gln Phe Thr Ser Glu Pro Val Gln Leu Thr Pro  
 365 370 375  
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 Asp Asp Glu Asp Ala Ile Lys Arg Ile Asp Gln Ser Glu Phe Glu Gly  
 380 385 390  
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 Phe Glu Tyr Ile Asn Pro Leu Leu Leu Ser Thr Glu Glu Ser Val  
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<210> 2  
 <211> 409  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> (27)  
 <223> Xaa at position 27 is Asp or Asn

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 Ser Ser Ser Arg Lys His Asp Ser Ile Lys Asp Asp Ser Glu Asp Leu  
 35 40 45  
 Lys Pro Val Ile Asp Gly Met Asp Gly Ile Lys Ile Ser Gln Gly Leu  
 50 55 60  
 Gly Leu Gln Asp Phe Asp Leu Ile Arg Val Ile Gly Arg Gly Ser Tyr  
 65 70 75 80  
 Ala Lys Val Leu Leu Val Arg Leu Lys Lys Asn Asp Gln Ile Tyr Ala  
 85 90 95

Met Lys Val Val Lys Lys Glu Leu Val His Asp Asp Glu Asp Ile Asp  
100 105 110  
Trp Val Gln Thr Glu Lys His Val Phe Glu Gln Ala Ser Ser Asn Pro  
115 120 125  
Phe Leu Val Gly Leu His Ser Cys Phe Gln Thr Thr Ser Arg Leu Phe  
130 135 140  
Leu Val Ile Glu Tyr Val Asn Gly Gly Asp Leu Met Phe His Met Gln  
145 150 155 160  
Arg Gln Arg Lys Leu Pro Glu Glu His Ala Arg Phe Tyr Ala Ala Glu  
165 170 175  
Ile Cys Ile Ala Leu Asn Phe Leu His Glu Arg Gly Ile Ile Tyr Arg  
180 185 190  
Asp Leu Lys Leu Asp Asn Val Leu Leu Asp Ala Asp Gly His Ile Lys  
195 200 205  
Leu Thr Asp Tyr Gly Met Cys Lys Glu Gly Leu Gly Pro Gly Asp Thr  
210 215 220  
Thr Ser Thr Phe Cys Gly Thr Pro Asn Tyr Ile Ala Pro Glu Ile Leu  
225 230 235 240  
Arg Gly Glu Glu Tyr Gly Phe Ser Val Asp Trp Trp Ala Leu Gly Val  
245 250 255  
Leu Met Phe Glu Met Met Ala Gly Arg Ser Pro Phe Asp Ile Ile Thr  
260 265 270  
Asp Asn Pro Asp Met Asn Thr Glu Asp Tyr Leu Phe Gln Val Ile Leu  
275 280 285  
Glu Lys Pro Ile Arg Ile Pro Arg Phe Leu Ser Val Lys Ala Ser His  
290 295 300  
Val Leu Lys Gly Phe Leu Asn Lys Asp Pro Lys Glu Arg Leu Gly Cys  
305 310 315 320  
Arg Pro Gln Thr Gly Phe Ser Asp Ile Lys Ser His Ala Phe Phe Arg  
325 330 335  
Ser Ile Asp Trp Asp Leu Leu Glu Lys Lys Gln Ala Leu Pro Pro Phe  
340 345 350  
Gln Pro Gln Ile Thr Asp Asp Tyr Gly Leu Asp Asn Phe Asp Thr Gln  
355 360 365  
Phe Thr Ser Glu Pro Val Gln Leu Thr Pro Asp Asp Glu Asp Ala Ile  
370 375 380  
Lys Arg Ile Asp Gln Ser Glu Phe Glu Gly Phe Glu Tyr Ile Asn Pro  
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<211> 2058

<212> DNA  
<213> Homo sapiens

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ttcggctgcg tcgtagtcca gcagttgccc ttctttctac ggagggacgt gcggggcggc 180  
cgtgtctcgt atttcttaga cgcgactcct ccgtcctctt ctttcggctt agatagatgg 240  
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tgggacggct ccccgacag tacgccaag gttccacgtg taaaagggtc ctttgtcttg 1980  
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<210> 4  
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<212> PRT  
<213> Unknown Organism

<220>  
<223> Description of Unknown Organism: mzip peptide

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